

His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		
				65					70					75		
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		
				80					85					90		
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		
				95					100					105		
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		
				110					115					120		
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		
				125					130					135		
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		
				140					145					150		
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		
				155					160					165		
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		
				170					175					180		
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		
				185					190					195		
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		
				200					205					210		
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		
				215					220					225		
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		
				230					235					240		
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		
				245					250					255		
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		
				260					265					270		
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		
				275					280					285		
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		
				290					295					300		
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		
				305					310					315		
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		
				320					325					330		
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		
				335					340					345		
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln		

Val Glu Asp Val	Asp Glu Pro Pro Leu	Phe Leu Leu Pro Tyr	Tyr
365		370	375
Val Phe Glu Val	Phe Glu Glu Thr Pro	Gln Gly Ser Phe Val	Gly
380		385	390
Val Val Ser Ala	Thr Asp Pro Asp Asn	Arg Lys Ser Pro Ile	Arg
395		400	405
Tyr Ser Ile Thr	Arg Ser Lys Val Phe	Asn Ile Asn Asp Asn	Gly
410		415	420
Thr Ile Thr Thr	Ser Asn Ser Leu Asp	Arg Glu Ile Ser Ala	Trp
425		430	435
Tyr Asn Leu Ser	Ile Thr Ala Thr Glu	Lys Tyr Asn Ile Glu	Gln
440		445	450
Ile Ser Ser Ile	Pro Leu Tyr Val Gln	Val Leu Asn Ile Asn	Asp
455		460	465
His Ala Pro Glu	Phe Ser Gln Tyr Tyr	Glu Thr Tyr Val Cys	Glu
470		475	480
Asn Ala Gly Ser	Gly Gln Val Ile Gln	Thr Ile Ser Ala Val	Asp
485		490	495
Arg Asp Glu Ser	Ile Glu Glu His His	Phe Tyr Phe Asn Leu	Ser
500		505	510
Val Glu Asp Thr	Asn Asn Ser Ser Phe	Thr Ile Ile Asp Asn	Gln
515		520	525
Asp Asn Thr Ala	Val Ile Leu Thr Asn	Arg Thr Gly Phe Asn	Leu
530		535	540
Gln Glu Glu Pro	Val Phe Tyr Ile Ser	Ile Leu Ile Ala Asp	Asn
545		550	555
Gly Ile Pro Ser	Leu Thr Ser Thr Asn	Thr Leu Thr Ile His	Val
560		565	570
Cys Asp Cys Gly	Asp Ser Gly Ser Thr	Gln Thr Cys Gln Tyr	Gln
575		580	585
Glu Leu Val Leu	Ser Met Gly Phe Lys	Thr Glu Val Ile Ile	Ala
590		595	600
Ile Leu Ile Cys	Ile Met Ile Ile Phe	Gly Phe Ile Phe Leu	Thr
605		610	615
Leu Gly Leu Lys	Gln Arg Arg Lys Gln	Ile Leu Phe Pro Glu	Lys
620		625	630
Ser Glu Asp Phe	Arg Glu Asn Ile Phe	Gln Tyr Asp Asp Glu	Gly
635		640	645

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg  
 650 655 660  
 Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser  
 665 670 675  
 Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro  
 680 685 690  
 Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu  
 695 700 705  
 Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr  
 710 715 720  
 Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser  
 725 730 735  
 Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu  
 740 745 750  
 Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly  
 755 760 765  
 Ser Ala Val Gln Ser Asn Asn  
 770

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 <211> 349  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 24, 60, 141, 226, 228, 249, 252  
 <223> unknown base

<400> 265  
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 gaatatttttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100  
 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150  
 aagtgtatta attaaacttt cagatgttaa tgacaataag cctatatatta 200  
 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250  
 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300  
 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

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 <211> 25  
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 <213> Artificial Sequence  
 <220>